



#6

SEQUENCE LISTING

<110> Allen, Keith D.

<120> TRANSGENIC MICE CONTAINING
MAGNESIUM-DEPENDENT PROTEIN PHOSPHATASE GENE DISRUPTIONS

<130> R-723-CIP

<140> US 09/972,741

<141> 2001-10-05

<150> US 09/815,935

<151> 2001-03-22

<150> US 60/191,235

<151> 2000-03-22

<150> US 60/216,249

<151> 2000-07-06

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1387

<212> DNA

<213> Mus musculus

<400> 1

```
cccgggcccg gccgcccgtcg egggaccccg tgccccggccg ccgtcgccac cgccgccccg 60
gccgaccgag ggacccgccc gcccgcggt gctccggacc tagaggatca agtcataatg 120
ggagcatttt tagacaagcc aaagatggag aagcataatg cccaggggca ggggaatggg 180
ttacgatacg gcctaagcag catgcaaggt tggcagagttg aaatggagga cgcacacacg 240
gctgtgatcg gtttgccaag tggacttgag acatgggtcat tctttgctgt atatgatggg 300
catgctgggt ctcagggtgc caaatactgc tgtgagcact tgtagatca catcaccaat 360
aaccaggatt tcagaggatc tgcaggagca ctttctgtgg agaacgtaaa gaatggaatc 420
agaacagggg ttctggagat tgatgaacac atgagagtta tgtagagaa gaaacatggg 480
gcagatagaa gcgggtcaac agctgtgggc gtcttaatct ctccccaaca tacttatttc 540
attaactgtg gagactcgag aggtttactt tgtaggaata gaaaagttca cttcttcaca 600
caagaccata aaccaagtaa cccgctggaa aaagaacgaa ttcagaatgc agggggctcg 660
gtgatgattc agcgtgtcaa tggctctctg gctgtatcga gggcccttgg ggatttcgat 720
tacaaatgtg tccatggaaa aggtcccaca gagcagcttg tctcccaga gcccgagtc 780
catgatattg aaaggtctga agaagatgac cagttcatca tccttgcag cgatggcatc 840
tgggacgtca tggggaacga agagctctgt gactttgtga gatccagact tgaagtcact 900
gatgaccttg agaaagtttg caatgaagta gtcgacacct gcttgataa gggaagtcga 960
gacaacatga gtgtgatttt gatctgtttt ccaagtgcac ccaaagtctc ggcagaggcg 1020
gtgaagaagg aggcggagct ggacaagtac ctggagagca gagtagaaga aatcataaag 1080
aagcaggtgg aaggcgtccc tgacttagtc cacgtgatgc gcacgttagc cagtgagaac 1140
atccccagcc tcccaccagg gggatgaattg gcaagcaagc ggaatgtaat tgaagccgtt 1200
tacaatagac tgaaccctta caaaaatgac gacactgatt ctgcgtcaac cgatgatatg 1260
tggtaaagcc gctcaccag ccgtggactc accttcgcct gcaaagggga agccagctca 1320
tccttgccga gcctttacca tccatcaccg acttcacagg aggggtctgac acgggtgagg 1380
actgcag
```

<210> 2

<211> 382

<212> PRT

<213> Mus musculus

<400> 2

Met	Gly	Ala	Phe	Leu	Asp	Lys	Pro	Lys	Met	Glu	Lys	His	Asn	Ala	Gln
1				5					10					15	
Gly	Gln	Gly	Asn	Gly	Leu	Arg	Tyr	Gly	Leu	Ser	Ser	Met	Gln	Gly	Trp
			20					25					30		
Arg	Val	Glu	Met	Glu	Asp	Ala	His	Thr	Ala	Val	Ile	Gly	Leu	Pro	Ser
		35					40					45			
Gly	Leu	Glu	Thr	Trp	Ser	Phe	Phe	Ala	Val	Tyr	Asp	Gly	His	Ala	Gly
	50					55					60				
Ser	Gln	Val	Ala	Lys	Tyr	Cys	Cys	Glu	His	Leu	Asp	His	Ile	Thr	
65					70					75				80	
Asn	Asn	Gln	Asp	Phe	Arg	Gly	Ser	Ala	Gly	Ala	Pro	Ser	Val	Glu	Asn
				85					90					95	
Val	Lys	Asn	Gly	Ile	Arg	Thr	Gly	Phe	Leu	Glu	Ile	Asp	Glu	His	Met
		100						105					110		
Arg	Val	Met	Ser	Glu	Lys	Lys	His	Gly	Ala	Asp	Arg	Ser	Gly	Ser	Thr
	115						120					125			
Ala	Val	Gly	Val	Leu	Ile	Ser	Pro	Gln	His	Thr	Tyr	Phe	Ile	Asn	Cys
	130					135						140			
Gly	Asp	Ser	Arg	Gly	Leu	Leu	Cys	Arg	Asn	Arg	Lys	Val	His	Phe	Phe
145					150					155					160
Thr	Gln	Asp	His	Lys	Pro	Ser	Asn	Pro	Leu	Glu	Lys	Glu	Arg	Ile	Gln
				165					170					175	
Asn	Ala	Gly	Gly	Ser	Val	Met	Ile	Gln	Arg	Val	Asn	Gly	Ser	Leu	Ala
		180						185					190		
Val	Ser	Arg	Ala	Leu	Gly	Asp	Phe	Asp	Tyr	Lys	Cys	Val	His	Gly	Lys
	195					200						205			
Gly	Pro	Thr	Glu	Gln	Leu	Val	Ser	Pro	Glu	Pro	Glu	Val	His	Asp	Ile
	210					215						220			
Glu	Arg	Ser	Glu	Glu	Asp	Asp	Gln	Phe	Ile	Ile	Leu	Ala	Cys	Asp	Gly
225				230						235					240
Ile	Trp	Asp	Val	Met	Gly	Asn	Glu	Glu	Leu	Cys	Asp	Phe	Val	Arg	Ser
				245					250					255	
Arg	Leu	Glu	Val	Thr	Asp	Asp	Leu	Glu	Lys	Val	Cys	Asn	Glu	Val	Val
		260						265					270		
Asp	Thr	Cys	Leu	Tyr	Lys	Gly	Ser	Arg	Asp	Asn	Met	Ser	Val	Ile	Leu
	275						280					285			
Ile	Cys	Phe	Pro	Ser	Ala	Pro	Lys	Val	Ser	Ala	Glu	Ala	Val	Lys	Lys
	290					295					300				
Glu	Ala	Glu	Leu	Asp	Lys	Tyr	Leu	Glu	Ser	Arg	Val	Glu	Glu	Ile	Ile
305				310						315				320	
Lys	Lys	Gln	Val	Glu	Gly	Val	Pro	Asp	Leu	Val	His	Val	Met	Arg	Thr
				325					330					335	
Leu	Ala	Ser	Glu	Asn	Ile	Pro	Ser	Leu	Pro	Pro	Gly	Gly	Glu	Leu	Ala
		340						345					350		
Ser	Lys	Arg	Asn	Val	Ile	Glu	Ala	Val	Tyr	Asn	Arg	Leu	Asn	Pro	Tyr
		355					360					365			
Lys	Asn	Asp	Asp	Thr	Asp	Ser	Ala	Ser	Thr	Asp	Asp	Met	Trp		
	370					375						380			

<210> 3

<211> 200

<212> DNA

<213> Artificial Sequence

<220>

<223> Targeting vector

<400> 3
gcaacacaat gcttgtaggt atagcctgtg agtttttcca gcttccttgt atcttataga 60
ttctgggtaa agagtgttgg acatgttttg tttcaaaggc aatcacttat tttcttattt 120
ctcttccttt acagacctag aggatcaagt cataatggga gcatttttag acaagccaaa 180
gatggagaag cataatgccc 200

<210> 4
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> Targeting vector

<400> 4
ctgctgtgag cacttggttag atcacatcac caataaccag gatttcagag gatctgcagg 60
agcaccttct gtggagaacg taaagaatgg aatcagaaca gggtttctgg agattgatga 120
acacatgaga gttatgtcag agaagaaaca tgggtgcagat agaagcgggt caacagctgt 180
gggcgtctta atctctcccc 200